

RAW SEQUENCE LISTING

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Application Serial Number: 10/820,712B
Source: 1Fw/6
Date Processed by STIC: 7/20/06

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IFW16

RAW SEQUENCE LISTING

DATE: 07/20/2006

PATENT APPLICATION: US/10/820,712B

TIME: 09:22:16

Input Set : A:\251701US0.ST25.txt

Output Set: N:\CRF4\07202006\J820712B.raw

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3 <110> APPLICANT: SATO, TSUYOSHI
4     OKUDA, MITSUYOSHI
5     KOYAMA, SHINGO
6     IZAWA, YOSHIFUMI
7     KOBAYASHI, TOHRU
9 <120> TITLE OF INVENTION: ALKALINE PROTEASE
11 <130> FILE REFERENCE: 251701US0
C--> 13 <140> CURRENT APPLICATION NUMBER: US/10/820,712B
14 <141> CURRENT FILING DATE: 2004-04-09
16 <150> PRIOR APPLICATION NUMBER: JP 2003-106708
17 <151> PRIOR FILING DATE: 2003-04-10
19 <160> NUMBER OF SEQ ID NOS: 24
21 <170> SOFTWARE: PatentIn version 3.3
23 <210> SEQ ID NO: 1
24 <211> LENGTH: 434
25 <212> TYPE: PRT
26 <213> ORGANISM: Bacillus sp. KSM-KP43
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31 1          5          10          15
34 Tyr Gly Leu Tyr Gly Gln Gly Gln Ile Val Ala Val Ala Asp Thr Gly
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38 Leu Asp Thr Gly Arg Asn Asp Ser Ser Met His Glu Ala Phe Arg Gly
39          35          40          45
42 Lys Ile Thr Ala Leu Tyr Ala Leu Gly Arg Thr Asn Asn Ala Asn Asp
43          50          55          60
46 Thr Asn Gly His Gly Thr His Val Ala Gly Ser Val Leu Gly Asn Gly
47 65          70          75          80
50 Ser Thr Asn Lys Gly Met Ala Pro Gln Ala Asn Leu Val Phe Gln Ser
51          85          90          95
54 Ile Met Asp Ser Gly Gly Gly Leu Gly Gly Leu Pro Ser Asn Leu Gln
55          100         105         110
58 Thr Leu Phe Ser Gln Ala Tyr Ser Ala Gly Ala Arg Ile His Thr Asn
59          115         120         125
62 Ser Trp Gly Ala Ala Val Asn Gly Ala Tyr Thr Thr Asp Ser Arg Asn
63          130         135         140
66 Val Asp Asp Tyr Val Arg Lys Asn Asp Met Thr Ile Leu Phe Ala Ala
67 145         150         155         160
70 Gly Asn Glu Gly Pro Asn Gly Gly Thr Ile Ser Ala Pro Gly Thr Ala
71          165         170         175
74 Lys Asn Ala Ile Thr Val Gly Ala Thr Glu Asn Leu Arg Pro Ser Phe
75          180         185         190
78 Gly Ser Tyr Ala Asp Asn Ile Asn His Val Ala Gln Phe Ser Ser Arg

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82 Gly Pro Thr Lys Asp Gly Arg Ile Lys Pro Asp Val Met Ala Pro Gly
83          210          215          220
86 Thr Phe Ile Leu Ser Ala Arg Ser Ser Leu Ala Pro Asp Ser Ser Phe
87 225          230          235          240
90 Trp Ala Asn His Asp Ser Lys Tyr Ala Tyr Met Gly Gly Thr Ser Met
91          245          250          255
94 Ala Thr Pro Ile Val Ala Gly Asn Val Ala Gln Leu Arg Glu His Phe
95          260          265          270
98 Val Lys Asn Arg Gly Ile Thr Pro Lys Pro Ser Leu Leu Lys Ala Ala
99          275          280          285
102 Leu Ile Ala Gly Ala Ala Asp Ile Gly Leu Gly Tyr Pro Asn Gly Asn
103          290          295          300
106 Gln Gly Trp Gly Arg Val Thr Leu Asp Lys Ser Leu Asn Val Ala Tyr
107 305          310          315          320
110 Val Asn Glu Ser Ser Ser Leu Ser Thr Ser Gln Lys Ala Thr Tyr Ser
111          325          330          335
114 Phe Thr Ala Thr Ala Gly Lys Pro Leu Lys Ile Ser Leu Val Trp Ser
115          340          345          350
118 Asp Ala Pro Ala Ser Thr Thr Ala Ser Val Thr Leu Val Asn Asp Leu
119          355          360          365
122 Asp Leu Val Ile Thr Ala Pro Asn Gly Thr Gln Tyr Val Gly Asn Asp
123          370          375          380
126 Phe Thr Ser Pro Tyr Asn Asp Asn Trp Asp Gly Arg Asn Asn Val Glu
127 385          390          395          400
130 Asn Val Phe Ile Asn Ala Pro Gln Ser Gly Thr Tyr Thr Ile Glu Val
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138 Val Asn
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143 <211> LENGTH: 1923
144 <212> TYPE: DNA
145 <213> ORGANISM: Bacillus sp. KSM-KP43
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150 <222> LOCATION: (1)..(1920)
152 <220> FEATURE:
153 <221> NAME/KEY: sig_peptide
154 <222> LOCATION: (1)..(618)
156 <220> FEATURE:
157 <221> NAME/KEY: mat_peptide
158 <222> LOCATION: (619)..(1920)
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165 gcg att ttg tcg act gtt gcg tta agt aat cca tct gca ggt ggt 90
166 Ala Ile Leu Ser Thr Val Ala Leu Ser Asn Pro Ser Ala Gly Gly

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169	gca agg aat ttt gat ctg gat ttc aaa gga att cag aca aca act	135		
170	Ala Arg Asn Phe Asp Leu Asp Phe Lys Gly Ile Gln Thr Thr Thr			
171	-175	-170	-165	
173	gat gct aaa ggt ttc tcc aag cag ggg cag act ggt gct gct gct	180		
174	Asp Ala Lys Gly Phe Ser Lys Gln Gly Gln Thr Gly Ala Ala Ala			
175	-160	-155	-150	
177	ttt ctg gtg gaa tct gaa aat gtg aaa ctc cca aaa ggt ttg cag	225		
178	Phe Leu Val Glu Ser Glu Asn Val Lys Leu Pro Lys Gly Leu Gln			
179	-145	-140	-135	
181	aag aag ctt gaa aca gtc ccg gca aat aat aaa ctc cat att atc	270		
182	Lys Lys Leu Glu Thr Val Pro Ala Asn Asn Lys Leu His Ile Ile			
183	-130	-125	-120	
185	caa ttc aat gga cca att tta gaa gaa aca aaa cag cag ctg gaa	315		
186	Gln Phe Asn Gly Pro Ile Leu Glu Glu Thr Lys Gln Gln Leu Glu			
187	-115	-110	-105	
189	aaa aca ggg gca aag att ctc gac tac ata cct gat tat gct tac att	363		
190	Lys Thr Gly Ala Lys Ile Leu Asp Tyr Ile Pro Asp Tyr Ala Tyr Ile			
191	-100	-95	-90	
193	gtc gag tat gag ggc gat gtt aag tca gca aca agc acc att gag cac	411		
194	Val Glu Tyr Glu Gly Asp Val Lys Ser Ala Thr Ser Thr Ile Glu His			
195	-85	-80	-75	-70
197	gtg gaa tcc gtg gag cct tat ttg ccg ata tac aga ata gat ccc cag	459		
198	Val Glu Ser Val Glu Pro Tyr Leu Pro Ile Tyr Arg Ile Asp Pro Gln			
199	-65	-60	-55	
201	ctt ttc aca aaa ggg gca tca gag ctt gta aaa gca gtg gcg ctt gat	507		
202	Leu Phe Thr Lys Gly Ala Ser Glu Leu Val Lys Ala Val Ala Leu Asp			
203	-50	-45	-40	
205	aca aag cag aaa aat aaa gag gtg caa tta aga ggc atc gaa caa atc	555		
206	Thr Lys Gln Lys Asn Lys Glu Val Gln Leu Arg Gly Ile Glu Gln Ile			
207	-35	-30	-25	
209	gca caa ttc gca ata agc aat gat gtg cta tat att acg gca aag cct	603		
210	Ala Gln Phe Ala Ile Ser Asn Asp Val Leu Tyr Ile Thr Ala Lys Pro			
211	-20	-15	-10	
213	gag tat aag gtg atg aat gat gtt gcg cgt gga att gtc aaa gcg gat	651		
214	Glu Tyr Lys Val Met Asn Asp Val Ala Arg Gly Ile Val Lys Ala Asp			
215	-5	-1	1	5
217	gtg gct cag agc agc tac ggg ttg tat gga caa gga cag atc gta gcg	699		
218	Val Ala Gln Ser Ser Tyr Gly Leu Tyr Gly Gln Gly Gln Ile Val Ala			
219	15	20	25	
221	gtt gcc gat aca ggg ctt gat aca ggt cgc aat gac agt tcg atg cat	747		
222	Val Ala Asp Thr Gly Leu Asp Thr Gly Arg Asn Asp Ser Ser Met His			
223	30	35	40	
225	gaa gcc ttc cgc ggg aaa att act gca tta tat gca ttg gga cgg acg	795		
226	Glu Ala Phe Arg Gly Lys Ile Thr Ala Leu Tyr Ala Leu Gly Arg Thr			
227	45	50	55	
229	aat aat gcc aat gat acg aat ggt cat ggt acg cat gtg gct ggc tcc	843		
230	Asn Asn Ala Asn Asp Thr Asn Gly His Gly Thr His Val Ala Gly Ser			
231	60	65	70	75

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234	Val	Leu	Gly	Asn	Gly	Ser	Thr	Asn	Lys	Gly	Met	Ala	Pro	Gln	Ala	Asn	
235				80					85					90			
237	cta	gtc	ttc	caa	tct	atc	atg	gat	agc	ggg	gga	ctt	gga	gga	cta		939
238	Leu	Val	Phe	Gln	Ser	Ile	Met	Asp	Ser	Gly	Gly	Gly	Leu	Gly	Gly	Leu	
239				95					100					105			
241	cct	tcg	aat	ctg	caa	acc	tta	ttc	agc	caa	gca	tac	agt	gct	ggg	gcc	987
242	Pro	Ser	Asn	Leu	Gln	Thr	Leu	Phe	Ser	Gln	Ala	Tyr	Ser	Ala	Gly	Ala	
243			110					115					120				
245	aga	att	cat	aca	aac	tcc	tgg	gga	gca	gca	gtg	aat	ggg	gct	tac	aca	1035
246	Arg	Ile	His	Thr	Asn	Ser	Trp	Gly	Ala	Ala	Val	Asn	Gly	Ala	Tyr	Thr	
247		125					130					135					
249	aca	gat	tcc	aga	aat	gtg	gat	gac	tat	gtg	cgc	aaa	aat	gat	atg	acg	1083
250	Thr	Asp	Ser	Arg	Asn	Val	Asp	Asp	Tyr	Val	Arg	Lys	Asn	Asp	Met	Thr	
251	140					145					150					155	
253	atc	ctt	ttc	gct	gcc	ggg	aat	gaa	gga	ccg	aac	ggc	gga	acc	atc	agt	1131
254	Ile	Leu	Phe	Ala	Ala	Gly	Asn	Glu	Gly	Pro	Asn	Gly	Gly	Thr	Ile	Ser	
255				160					165					170			
257	gca	cca	ggc	aca	gct	aaa	aat	gca	ata	aca	gtc	gga	gct	acg	gaa	aac	1179
258	Ala	Pro	Gly	Thr	Ala	Lys	Asn	Ala	Ile	Thr	Val	Gly	Ala	Thr	Glu	Asn	
259				175				180						185			
261	ctc	cgc	cca	agc	ttt	ggg	tct	tat	gcg	gac	aat	atc	aac	cat	gtg	gca	1227
262	Leu	Arg	Pro	Ser	Phe	Gly	Ser	Tyr	Ala	Asp	Asn	Ile	Asn	His	Val	Ala	
263			190					195					200				
265	cag	ttc	tct	tca	cgt	gga	ccg	aca	aag	gat	gga	cgg	atc	aaa	ccg	gat	1275
266	Gln	Phe	Ser	Ser	Arg	Gly	Pro	Thr	Lys	Asp	Gly	Arg	Ile	Lys	Pro	Asp	
267		205					210					215					
269	gtc	atg	gca	ccg	gga	acg	ttc	ata	cta	tca	gca	aga	tct	tct	ctt	gca	1323
270	Val	Met	Ala	Pro	Gly	Thr	Phe	Ile	Leu	Ser	Ala	Arg	Ser	Ser	Leu	Ala	
271	220					225					230					235	
273	ccg	gat	tcc	tcc	ttc	tgg	gcg	aac	cat	gac	agt	aaa	tat	gca	tac	atg	1371
274	Pro	Asp	Ser	Ser	Phe	Trp	Ala	Asn	His	Asp	Ser	Lys	Tyr	Ala	Tyr	Met	
275				240					245					250			
277	ggg	gga	acg	tcc	atg	gct	aca	ccg	atc	ggt	gct	gga	aac	gtg	gca	cag	1419
278	Gly	Gly	Thr	Ser	Met	Ala	Thr	Pro	Ile	Val	Ala	Gly	Asn	Val	Ala	Gln	
279				255				260						265			
281	ctt	cgt	gag	cat	ttt	gtg	aaa	aac	aga	ggc	atc	aca	cca	aag	cct	tct	1467
282	Leu	Arg	Glu	His	Phe	Val	Lys	Asn	Arg	Gly	Ile	Thr	Pro	Lys	Pro	Ser	
283			270					275						280			
285	cta	tta	aaa	gcg	gca	ctg	att	gcc	ggg	gca	gct	gac	atc	ggc	ctt	ggc	1515
286	Leu	Leu	Lys	Ala	Ala	Leu	Ile	Ala	Gly	Ala	Ala	Asp	Ile	Gly	Leu	Gly	
287		285				290						295					
289	tac	ccg	aac	ggg	aac	caa	gga	tgg	gga	cga	gtg	aca	ttg	gat	aaa	tcc	1563
290	Tyr	Pro	Asn	Gly	Asn	Gln	Gly	Trp	Gly	Arg	Val	Thr	Leu	Asp	Lys	Ser	
291	300					305					310					315	
293	ctg	aac	ggt	gcc	tat	gtg	aac	gag	tcc	agt	tct	cta	tcc	acc	agc	caa	1611
294	Leu	Asn	Val	Ala	Tyr	Val	Asn	Glu	Ser	Ser	Ser	Leu	Ser	Thr	Ser	Gln	
295				320					325					330			
297	aaa	gcg	acg	tac	tcg	ttt	act	gct	act	gcc	ggc	aag	cct	ttg	aaa	atc	1659

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298 Lys Ala Thr Tyr Ser Phe Thr Ala Thr Ala Gly Lys Pro Leu Lys Ile
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302 Ser Leu Val Trp Ser Asp Ala Pro Ala Ser Thr Thr Ala Ser Val Thr
303          350          355          360
305 ctt gtc aat gat ctg gac ctt gtc att acc gct cca aat ggc aca cag      1755
306 Leu Val Asn Asp Leu Asp Leu Val Ile Thr Ala Pro Asn Gly Thr Gln
307          365          370          375
309 tat gta gga aat gac ttt act tcg cca tac aat gat aac tgg gat ggc      1803
310 Tyr Val Gly Asn Asp Phe Thr Ser Pro Tyr Asn Asp Asn Trp Asp Gly
311 380          385          390          395
313 cgc aat aac gta gaa aat gta ttt att aat gca cca caa agc ggg acg      1851
314 Arg Asn Asn Val Glu Asn Val Phe Ile Asn Ala Pro Gln Ser Gly Thr
315          400          405          410
317 tat aca att gag gta cag gct tat aac gta ccg gtt gga cca cag acc      1899
318 Tyr Thr Ile Glu Val Gln Ala Tyr Asn Val Pro Val Gly Pro Gln Thr
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342 -175          -170          -165
345 Asp Ala Lys Gly Phe Ser Lys Gln Gly Gln Thr Gly Ala Ala Ala
346 -160          -155          -150
349 Phe Leu Val Glu Ser Glu Asn Val Lys Leu Pro Lys Gly Leu Gln
350 -145          -140          -135
353 Lys Lys Leu Glu Thr Val Pro Ala Asn Asn Lys Leu His Ile Ile
354 -130          -125          -120
357 Gln Phe Asn Gly Pro Ile Leu Glu Glu Thr Lys Gln Gln Leu Glu
358 -115          -110          -105
361 Lys Thr Gly Ala Lys Ile Leu Asp Tyr Ile Pro Asp Tyr Ala Tyr Ile
362 -100          -95          -90
365 Val Glu Tyr Glu Gly Asp Val Lys Ser Ala Thr Ser Thr Ile Glu His
366 -85          -80          -75          -70
369 Val Glu Ser Val Glu Pro Tyr Leu Pro Ile Tyr Arg Ile Asp Pro Gln
370          -65          -60          -55
373 Leu Phe Thr Lys Gly Ala Ser Glu Leu Val Lys Ala Val Ala Leu Asp
374          -50          -45          -40
377 Thr Lys Gln Lys Asn Lys Glu Val Gln Leu Arg Gly Ile Glu Gln Ile
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